

SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company
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 <151> 1999-01-27
 <150> 60/144,783
 <151> 1999-07-20
 <150> 60/156,094
 <151> 1999-09-24
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 <211> 1756
 <212> DNA
 <213> Glycine max

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 gcactcatcg atctctccaa aaagcatggc cccttattct ctctctcctt cgggtccatg 300
 ccaaccgtcg ttgcctccac ccctgagttg ttcaagctct tcctccaaac ccacgaggca 360
 acttccttca acacaagggt ccaaacctct gccataagac gcctcactta cgacaactct 420
 gtggccatgg ttccattcgg accttactgg aagttcgtga ggaagctcat catgaacgac 480
 cttctcaacg ccaccaccgt caacaagctc aggcctttga ggacccaaca gatccgcaag 540
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 agagacatcg ctgcgaggt tcttaagatc ttcggcgaat acagcctcac tgacttcatc 720
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 gtcgactttt tctctgcagg gacagattcc acagcgggtg caacagagtg ggcattggca 1020
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 gtgaaggaga cattccgaat gcacccacca ctcccagtg tcaaaagaaa gtgcacagaa 1200
 gagtgtgaga ttaatgggta tgtgatccca gagggagcat tggttctttt caatgtttgg 1260
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 gttccaaggg cacatagtct cgttttgtgt ccacttgcaa ggatcggcgt tgcattctaa 1620
 ctctttctt aattaagata atcatcatat acaatagtag tgtcttgcca tcgcagttgc 1680
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 aaggttacat acatgc 1756

<210> 2
 <211> 521
 <212> PRT
 <213> Glycine max

<400> 2

Met Leu Leu Glu Leu Ala Leu Gly Leu Phe Val Leu Ala Leu Phe Leu
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 20 25 30
 Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
 35 40 45
 His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
 50 55 60
 Lys Lys His Gly Pro Leu Phe Ser Leu Ser Phe Gly Ser Met Pro Thr
 65 70 75 80
 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
 85 90 95
 Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
 100 105 110
 Leu Thr Tyr Asp Asn Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
 115 120 125
 Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
 130 135 140
 Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys Phe Leu
 145 150 155 160
 Arg Val Met Ala Gln Ser Ala Glu Ala Gln Lys Pro Leu Asp Val Thr
 165 170 175
 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
 180 185 190
 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
 195 200 205
 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys Tyr Leu
 210 215 220
 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
 225 230 235 240
 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
 245 250 255
 Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Ala Ser Gly Val Phe
 260 265 270
 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
 275 280 285
 Ile Thr Lys Glu Gln Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
 290 295 300
 Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
 305 310 315 320
 Ile Asn Asn Pro Arg Val Leu Gln Lys Ala Arg Glu Glu Val Tyr Ser
 325 330 335
 Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
 340 345 350

Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
 355 360 365

Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
 370 375 380

Tyr Val Ile Pro Glu Gly Ala Leu Val Leu Phe Asn Val Trp Gln Val
 385 390 395 400

Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
 405 410 415

Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
 420 425 430

Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
 435 440 445

Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
 450 455 460

Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
 465 470 475 480

Ile Leu Lys Gly Asp Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
 485 490 495

Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
 500 505 510

Ile Gly Val Ala Ser Lys Leu Leu Ser
 515 520

<210> 3
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligonucleotide

<400> 3
 cgggatccat gcaaccggaa accgtcg

27

<210> 4
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligonucleotide

<400> 4
 ccggaattct caccaaaccat cacggaggta tc

32

<210> 5
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligonucleotide

<400> 5
 tcaaggagaa aaaaccccg atccatgttg ctggaacttg cacttgg

47

<210> 6
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligonucleotide

<400> 6
 ggccagtga ttgtaatacg actcactata gggcg 35

<210> 7
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 7
 aaaattagcc tcacaaaagc aaag 24

<210> 8
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 8
 atataaggat tgatagttaa tagtagg 27

<210> 9
 <211> 1824
 <212> DNA
 <213> Glycine max

<400> 9
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 ctgcaaaatc aaaagcactt cgccatctcc caaaccaccc aagcccaaaag cctcgtcttc 180
 ccttcatagg acaccttcat ctcttaaaag acaaacttct ccactacgca ctcatcgacc 240
 tctccaaaaa acatgggtccc ttattctctc tctacttttg ctccatgcca accgttgttg 300
 cctccacacc agaattgttc aaagtcttcc tccaaacgca cgaggcaact tccttcaaca 360
 caaggttcca aacctcagcc ataagacgcc tcacctatga tagctcagtg gccatgggtc 420
 ccttcggacc ttactggaag ttcgtgagga agctcatcat gaacgacctt cccaacgcca 480
 ccaactgtaa caagttgagg cctttgagga cccaacagac ccgcaagttc cttaggggta 540
 tggcccaagg cgcagaggca cagaagcccc ttgacttgac cgaggagctt ctgaaatgga 600
 ccaacagcac catctccatg atgatgctcg gcgaggctga ggagatcaga gacatcgctc 660
 gcgaggttct taagatcttt ggcgaatata gcctcactga cttcatctgg ccattgaagc 720
 atctcaaggt tggaaagtat gagaagagga tcgacgacat cttgaacaag ttcgaccctg 780
 tcgttgaaag ggtcatcaag aagcgccgtg agatcgtgag gaggagaaag aacggagagg 840
 ttgttgaggg tgaggtcagc ggggttttcc ttgacacttt gcttgaattc gctgaggatg 900
 agaccatgga gatcaaaatc accaaggacc acatcgaggg tcttgttgtc gactttttct 960
 cggcaggaac agactccaca gcggtggcaa cagagtgggc attggcagaa ctcatcaaca 1020
 atcctaaggt gttggaaaag gctcgtgagg aggtctacag tgttgtggga aaggacagac 1080
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 atggatatgt gatcccagag ggagcattga ttctcttcaa tgtatggcaa gtaggaagag 1260
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 ctgaagggga agcagggcct cttgatctta ggggacaaca ttttcaactt ctcccatttg 1380
 ggtctgggag gagaatgtgc cctggagtca atctggctac ttcgggaatg gcaacacttc 1440
 ttgcatctct tattcagtg cttcacttgc aagtgtctgg tccacaagga cagatattga 1500
 aggggtgtga cgccaaaagt agcatggaag agagagccgg cctcactgtt ccaagggcac 1560

atagtcttgt ctgtgttcca cttgcaagga tcggcgttgc atctaaactc ctttcttaat 1620
 taagatcatc atcatatata atatttactt tttgtgtgtt gataatcatc atttcaataa 1680
 ggtctcgttc atctactttt tatgaagtat ataagccctt ccatgcacat tgtatcatct 1740
 cccatttgc ttcgtttgct acctaaggca atcttttttt ttttagaate acatcatcct 1800
 actataaact atcaatcctt atat 1824

<210> 10
 <211> 521
 <212> PRT
 <213> Glycine max

<400> 10

Met Leu Leu Glu Leu Ala Leu Gly Leu Leu Val Leu Ala Leu Phe Leu
 1 5 10 15
 His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu
 20 25 30
 Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
 35 40 45
 His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
 50 55 60
 Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
 65 70 75 80
 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
 85 90 95
 Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
 100 105 110
 Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
 115 120 125
 Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Pro Asn Ala Thr Thr
 130 135 140
 Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Thr Arg Lys Phe Leu
 145 150 155 160
 Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
 165 170 175
 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
 180 185 190
 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
 195 200 205
 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
 210 215 220
 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
 225 230 235 240
 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
 245 250 255
 Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
 260 265 270
 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
 275 280 285

Ile Thr Lys Asp His Ile Glu Gly Leu Val Val Asp Phe Phe Ser Ala
 290 295 300
 Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
 305 310 315 320
 Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser
 325 330 335
 Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
 340 345 350
 Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
 355 360 365
 Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
 370 375 380
 Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
 385 390 395 400
 Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
 405 410 415
 Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
 420 425 430
 Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
 435 440 445
 Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
 450 455 460
 Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
 465 470 475 480
 Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
 485 490 495
 Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
 500 505 510
 Ile Gly Val Ala Ser Lys Leu Leu Ser
 515 520

<210> 11
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 11
 atgttgctgg aacttgcaact t

21

<210> 12
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 12
 ttaagaaagg agttagatg caacg

25

<210> 13
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 13
 tgtttctgca cttgcgtccc ac

22

<210> 14
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 14
 ccgataccttg caagtggaaac ac

22

<210> 15
 <211> 1501
 <212> DNA
 <213> Medicago sativa

<400> 15
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 accccccaag cccaaagcct cgtcttcctt tcattggcca ccttcacctc ttaaaagata 120
 aacttctcca ctatgcactc atcgatctct ccaaaaagca tggcccctta ttctctctct 180
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 acgtcaccga ggagcttctc aaatggacca acagcaccat ctccatgatg atgctcggcg 540
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 tcgtcagaag gagagagaac ggagaagtgt ttgaggcgga ggccagcggc gtcttcctcg 780
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 gaaagtgcac agaagagtgt gagattaatg ggtatgtgat ccagaggga gcattgggtc 1140
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 gtcccgagag gttcttagaa actggtgctg aaggggaagc agggcctctt gatcttaggg 1260
 gccagcattt ccaactcctc ccatttgggt ctgggaggag aatgtgccct ggtgtcaatt 1320
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 tgctgggccc tcaaggacaa atattgaaag gtgatgatgc caaagttagc atggaagaga 1440
 gagctggcct cacagttcca agggcacata gtctcgttg tgttcactt gcaaggatcg 1500
 g 1501

<210> 16
 <211> 499
 <212> PRT
 <213> Medicago sativa

<400> 16
 Phe Leu His Leu Arg Pro Thr Pro Ser Ala Lys Ser Lys Ala Leu Arg
 1 5 10 15

His Leu Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly
 20 25 30
 His Leu His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp
 35 40 45
 Leu Ser Lys Lys His Gly Pro Leu Phe Ser Leu Ser Phe Gly Ser Met
 50 55 60
 Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln
 65 70 75 80
 Thr His Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Thr
 85 90 95
 Arg Arg Leu Thr Tyr Asp Asn Ser Val Ala Met Val Pro Phe Gly Pro
 100 105 110
 Tyr Trp Arg Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala
 115 120 125
 Thr Thr Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys
 130 135 140
 Phe Leu Arg Val Met Ala Gln Ser Ala Glu Ala Gln Lys Pro Leu Asp
 145 150 155 160
 Val Thr Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met
 165 170 175
 Met Leu Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu
 180 185 190
 Lys Ile Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys
 195 200 205
 Tyr Leu Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn
 210 215 220
 Lys Phe Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Gly Ile
 225 230 235 240
 Val Arg Arg Arg Glu Asn Gly Glu Val Val Glu Gly Glu Ala Ser Gly
 245 250 255
 Val Phe Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu
 260 265 270
 Ile Lys Ile Thr Lys Glu Gln Ile Lys Gly Leu Val Val Asp Leu Phe
 275 280 285
 Ser Ala Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala
 290 295 300
 Glu Leu Ile Asn Asn Pro Arg Val Leu Gln Lys Ala Arg Glu Glu Val
 305 310 315 320
 Tyr Ser Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln
 325 330 335
 Asn Leu Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His
 340 345 350
 Pro Pro Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile
 355 360 365

Asn Gly Tyr Val Ile Pro Glu Gly Ala Leu Val Leu Phe Asn Val Trp
 370 375 380

Gln Val Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg
 385 390 395 400

Pro Glu Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu
 405 410 415

Asp Leu Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg
 420 425 430

Arg Met Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu
 435 440 445

Leu Ala Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln
 450 455 460

Gly Gln Ile Leu Lys Gly Asp Asp Ala Lys Val Ser Met Glu Glu Arg
 465 470 475 480

Ala Gly Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu
 485 490 495

Ala Arg Ile

<210> 17
 <211> 1501
 <212> DNA
 <213> Vicia villosa

<400> 17
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 aacttctcca ctacgcactc atcgacctct ccaaaaaaca tggctccctta ttctctctct 180
 actttggctc catgccaaac gttgttgccct ccacaccaga attgttcaag ctcttccctcc 240
 aaacgcacga ggcaacttcc ttcaacacaa gggtccaaac ctgagccata agacgcctca 300
 cctatgatag cttagtggcc atgggtccct tgggacctta ctggaagttc gtgaggaagc 360
 tcatcatgaa cgaccttctc aacgccacca ctgtaaacaa gttgaggcct ttgaggacct 420
 aacagatccg caagtccctt aggggttatgg cccaaggcgc agaggcacag aagccccttg 480
 acttgaccga ggagcttctg aaatggacca acagcaccat ctctatgatg atgctcggcg 540
 aggctgagga gatcagagac atcgctcgcg aggttcttaa gatctatggc gaatacagcc 600
 tcaactgact catctggcca ttgaagcatc tcaagggttg aaagtatgag aagaggatcg 660
 acgacatctt gaacaagttc gacctgtcg ttgaaagagt catcaagaag cgccgtgaga 720
 tcgtgaggag gagaaagaac ggagaggttg ttgagggtga ggtcagcggg gttttccttg 780
 acactttgct tgaattcgct gaggatgaga ccacggagat caaaatcacc aaggaccaca 840
 tcaagggtct tgttgtcgac tttttctcgg caggaaataga ctccacagcg gtggcaacag 900
 agtgggcatt ggcagaactc atcaacaatc ctaagggtgt ggaaaaggct cgtgaggagg 960
 tctacagtgt tgtgggaaag gacagacttg tggacgaagt tgacactcaa aaccttccct 1020
 acattagagc aatcgtgaag gagacattcc gcatgcaccc gccactccca gtggtcaaaa 1080
 gaaagtgcac agaagagtgt gagattaatg gatattgtat ccagagaggga gcattgattc 1140
 tcttcaatgt atggcaagta ggaagggacc ccaaatactg ggacagacca tcggagtgtc 1200
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 gacaacattt tcaacttctc ccatttgggt ctgggagggg aatgtgccct ggagtcaatc 1320
 tggctacttc gggaatggca acacttcttg catctcttat tcagtgtctt gacttgcaag 1380
 tgctgggtcc acaaggacag atattgaagg gtggtgacgc caaagtttagc atggaagaga 1440
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 g 1501

<210> 18
 <211> 499
 <212> PRT
 <213> Vicia villosa

<400> 18

Phe Leu His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg
 1 5 10 15
 His Leu Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly
 20 25 30
 His Leu His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp
 35 40 45
 Leu Ser Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met
 50 55 60
 Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln
 65 70 75 80
 Thr His Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile
 85 90 95
 Arg Arg Leu Thr Tyr Asp Ser Leu Val Ala Met Val Pro Phe Gly Pro
 100 105 110
 Tyr Trp Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala
 115 120 125
 Thr Thr Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys
 130 135 140
 Phe Leu Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp
 145 150 155 160
 Leu Thr Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met
 165 170 175
 Met Leu Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu
 180 185 190
 Lys Ile Tyr Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys
 195 200 205
 His Leu Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn
 210 215 220
 Lys Phe Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile
 225 230 235 240
 Val Arg Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly
 245 250 255
 Val Phe Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Thr Glu
 260 265 270
 Ile Lys Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe
 275 280 285
 Ser Ala Gly Ile Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala
 290 295 300
 Glu Leu Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val
 305 310 315 320
 Tyr Ser Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln
 325 330 335
 Asn Leu Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His
 340 345 350

Pro Pro Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile
 355 360 365

Asn Gly Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp
 370 375 380

Gln Val Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg
 385 390 395 400

Pro Glu Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Arg Pro Leu
 405 410 415

Asp Leu Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg
 420 425 430

Gly Met Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu
 435 440 445

Leu Ala Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln
 450 455 460

Gly Gln Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg
 465 470 475 480

Ala Gly Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu
 485 490 495

Ala Arg Ile

<210> 19
 <211> 1501
 <212> DNA
 <213> Lens culinaris

<400> 19
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 tgctgggccc tcaaggacaa atattgaaag gtgatgatgc caaagttagc atggaagaga 1440
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<210> 20
 <211> 499

<212> PRT
<213> Lens culinaris

<400> 20

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Phe Leu His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg
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His Leu Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly
          20           25           30

His Pro His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp
      35           40           45

Leu Ser Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met
 50           55           60

Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln
 65           70           75           80

Thr His Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile
          85           90           95

Arg Arg Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro
      100           105           110

Tyr Trp Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala
 115           120           125

Thr Thr Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys
 130           135           140

Phe Leu Arg Val Met Ala Gln Ser Ala Glu Ala Gln Lys Pro Leu Asp
 145           150           155           160

Val Thr Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met
      165           170           175

Met Leu Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu
 180           185           190

Lys Ile Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys
 195           200           205

Tyr Leu Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn
 210           215           220

Lys Phe Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile
 225           230           235           240

Val Arg Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Ala Ser Gly
      245           250           255

Val Phe Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu
 260           265           270

Ile Lys Ile Thr Lys Glu Gln Ile Lys Gly Leu Val Val Asp Phe Phe
 275           280           285

Ser Ala Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala
 290           295           300

Glu Leu Ile Asn Asn Pro Arg Val Leu Gln Lys Ala Arg Glu Glu Val
 305           310           315           320

Tyr Ser Val Val Gly Lys Asp Ile Leu Val Asp Glu Val Asp Thr Gln
      325           330           335

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Asn Leu Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His
340 345 350

Pro Pro Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile
355 360 365

Asn Gly His Val Ile Pro Glu Gly Ala Leu Val Leu Phe Asn Val Trp
370 375 380

Gln Val Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg
385 390 395 400

Pro Glu Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu
405 410 415

Asp Leu Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg
420 425 430

Arg Met Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu
435 440 445

Leu Ala Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln
450 455 460

Gly Gln Ile Leu Lys Gly Asp Asp Ala Lys Val Ser Met Glu Glu Arg
465 470 475 480

Ala Gly Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu
485 490 495

Ala Arg Ile

<210> 21
<211> 1501
<212> DNA
<213> Lens culinaris

<400> 21

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actttggctc	catgccaaac	gttggttgct	ccacaccaga	attggttcaag	ctcttccctcc	240
aaacgcacga	ggcaacttcc	ttcaacacaa	ggttccaaac	ctcagccata	agacgcctca	300
cctatgatag	ctcagtggtc	atgggttccct	tgggacctta	ctggaagtgc	gtgaggaagc	360
tcatcatgaa	cgaccttctc	aacgccacca	ctgtaaaca	gttgaggcct	ttgaggacct	420
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tactgactt	catctggcca	ttgaagcatc	tcaagggttg	aaagtatgag	aagaggatcg	660
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tcgtgaggag	gagaaagaac	ggagagggtg	ttgagggtga	ggtcagcggg	gttttccttg	780
acactttgct	tgaattcgct	gaggatgaga	ccatggagat	caaaatcacc	aaggaccaca	840
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agtgggcatt	ggcagaactc	atcaacaatc	ctaagggtgt	ggaaaaggct	cgtgaggagg	960
tctacagtgt	tgtgggaaag	gacagacttg	tggacgaagt	tgacactcaa	aaccttccct	1020
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<210> 22
 <211> 499
 <212> PRT
 <213> Lens culinaris

<400> 22

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 His Leu His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp
 35 40 45
 Leu Ser Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met
 50 55 60
 Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln
 65 70 75 80
 Thr His Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile
 85 90 95
 Arg Arg Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro
 100 105 110
 Tyr Trp Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala
 115 120 125
 Thr Thr Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys
 130 135 140
 Phe Leu Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp
 145 150 155 160
 Leu Thr Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met
 165 170 175
 Val Leu Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu
 180 185 190
 Lys Ile Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys
 195 200 205
 His Leu Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn
 210 215 220
 Lys Phe Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile
 225 230 235 240
 Val Arg Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly
 245 250 255
 Val Phe Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu
 260 265 270
 Ile Lys Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe
 275 280 285
 Ser Ala Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala
 290 295 300
 Glu Leu Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val
 305 310 315 320

Tyr Ser Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln
 325 330 335
 Asn Leu Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His
 340 345 350
 Pro Pro Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile
 355 360 365
 Asn Gly Cys Val Thr Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp
 370 375 380
 Gln Val Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg
 385 390 395 400
 Pro Glu Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Arg Pro Leu
 405 410 415
 Asp Leu Arg Gly Arg His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg
 420 425 430
 Arg Met Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu
 435 440 445
 Leu Ala Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln
 450 455 460
 Gly Gln Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg
 465 470 475 480
 Ala Gly Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu
 485 490 495
 Ala Arg Ile

<210> 23
 <211> 1566
 <212> DNA
 <213> Phaseolus aureus

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 ttcaacacaa gggtccaaac ctcagccata agacgcctca cctatgatag ctcagtggcc 360
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<210> 24
 <211> 522
 <212> PRT
 <213> Phaseolus aureus

<400> 24
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 Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
 35 40 45
 His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
 50 55 60
 Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
 65 70 75 80
 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
 85 90 95
 Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
 100 105 110
 Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
 115 120 125
 Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
 130 135 140
 Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys Phe Leu
 145 150 155 160
 Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
 165 170 175
 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
 180 185 190
 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
 195 200 205
 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
 210 215 220
 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
 225 230 235 240
 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
 245 250 255
 Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
 260 265 270
 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
 275 280 285

Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
290 295 300

Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
305 310 315 320

Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Ala Tyr Ser
325 330 335

Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
340 345 350

Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
355 360 365

Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
370 375 380

Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
385 390 395 400

Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
405 410 415

Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Arg Pro Leu Asp Leu
420 425 430

Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
435 440 445

Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
450 455 460

Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
465 470 475 480

Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
485 490 495

Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
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Ile Gly Val Ala Ser Lys Leu Leu Ser Lys
515 520

<210> 25
<211> 1566
<212> DNA
<213> Phaseolus aureus

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<210> 26
 <211> 521
 <212> PRT
 <213> Phaseolus aureus

<400> 26

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             20             25             30

Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
      35             40             45

His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
      50             55             60

Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
      65             70             75             80

Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
             85             90             95

Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
      100             105             110

Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
      115             120             125

Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
      130             135             140

Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys Phe Leu
      145             150             155             160

Arg Ala Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
             165             170             175

Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
      180             185             190

Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
      195             200             205

Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
      210             215             220

Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
      225             230             235             240

Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
             245             250             255

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Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
260 265 270

Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
275 280 285

Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
290 295 300

Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
305 310 315 320

Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser
325 330 335

Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
340 345 350

Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
355 360 365

Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
370 375 380

Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
385 390 395 400

Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
405 410 415

Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Arg Pro Leu Asp Leu
420 425 430

Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
435 440 445

Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
450 455 460

Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
465 470 475 480

Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
485 490 495

Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
500 505 510

Ile Gly Val Ala Ser Lys Leu Leu Ser
515 520

<210> 27
<211> 1566
<212> DNA
<213> Phaseolus aureus

<400> 27
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<210> 28
<211> 521
<212> PRT
<213> Phaseolus aureus

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<400> 28
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His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu
      20             25             30
Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
      35             40             45
His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
      50             55             60
Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
      65             70             75             80
Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
      85             90             95
Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
      100            105            110
Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
      115            120            125
Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
      130            135            140
Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys Phe Leu
      145            150            155            160
Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
      165            170            175
Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
      180            185            190
Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
      195            200            205

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Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
 210 215 220
 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
 225 230 235 240
 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
 245 250 255
 Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
 260 265 270
 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Thr Glu Ile Lys
 275 280 285
 Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
 290 295 300
 Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
 305 310 315 320
 Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser
 325 330 335
 Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
 340 345 350
 Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
 355 360 365
 Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
 370 375 380
 Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
 385 390 395 400
 Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
 405 410 415
 Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Arg Pro Leu Asp Leu
 420 425 430
 Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
 435 440 445
 Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
 450 455 460
 Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
 465 470 475 480
 Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
 485 490 495
 Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
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 Ile Gly Val Ala Ser Lys Leu Leu Ser
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<210> 29
 <211> 1566
 <212> DNA
 <213> Phaseolus aureus

<400> 29

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atcgacctct ccaaaaaaca tggtcctta ttctctctct actttggctc catgccaacc 240
gttggtgcct ccacaccaga attgttcaag ctcttctctc aaacgcacga ggcaacttcc 300
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gaccctgtcg ttgaaagagt catcaagaag cgccgtgaga tcgtgaggag gagaagaac 780
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gagattaatg gatattgat cccagaggga gcattgattc tcttcaatgt atggcaagta 1200
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<210> 30

<211> 521

<212> PRT

<213> Phaseolus aureus

<400> 30

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Met Leu Leu Glu Leu Ala Leu Gly Leu Leu Val Leu Ala Leu Phe Leu
  1             5             10             15

His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu
      20             25             30

Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
      35             40             45

His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
      50             55             60

Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
      65             70             75             80

Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
      85             90             95

Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
      100            105            110

Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
      115            120            125

Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
      130            135            140

Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys Phe Leu
      145            150            155            160

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Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
 165 170 175
 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
 180 185 190
 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
 195 200 205
 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
 210 215 220
 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
 225 230 235 240
 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
 245 250 255
 Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
 260 265 270
 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
 275 280 285
 Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
 290 295 300
 Gly Thr Asp Ser Thr Ala Glu Ala Thr Glu Trp Ala Leu Ala Glu Leu
 305 310 315 320
 Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser
 325 330 335
 Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
 340 345 350
 Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
 355 360 365
 Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
 370 375 380
 Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
 385 390 395 400
 Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
 405 410 415
 Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Arg Pro Leu Asp Leu
 420 425 430
 Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
 435 440 445
 Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
 450 455 460
 Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
 465 470 475 480
 Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
 485 490 495
 Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
 500 505 510

Ile Gly Val Ala Ser Lys Leu Leu Ser
515 520

<210> 31
<211> 1566
<212> DNA
<213> Trifolium pratense

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atcgctcgcg aggttcttaa gatctttggc gaatacacgc tcaactgactt catctggcca 660
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tcttaa 1566

<210> 32
<211> 521
<212> PRT
<213> Trifolium pratense

<400> 32
Met Leu Leu Glu Leu Ala Leu Gly Leu Leu Val Leu Ala Leu Phe Leu
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His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu
20 25 30
Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
35 40 45
His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
50 55 60
Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
65 70 75 80
Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
85 90 95
Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
100 105 110
Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Ile Gly Pro Tyr Trp
115 120 125

Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
 130 135 140
 Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys Phe Leu
 145 150 155 160
 Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
 165 170 175
 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
 180 185 190
 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
 195 200 205
 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
 210 215 220
 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
 225 230 235 240
 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
 245 250 255
 Arg Arg Lys Asn Gly Glu Val Asp Glu Gly Glu Val Ser Gly Val Phe
 260 265 270
 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Thr Glu Ile Lys
 275 280 285
 Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
 290 295 300
 Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
 305 310 315 320
 Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser
 325 330 335
 Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
 340 345 350
 Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
 355 360 365
 Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
 370 375 380
 Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
 385 390 395 400
 Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
 405 410 415
 Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Arg Pro Leu Asp Leu
 420 425 430
 Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
 435 440 445
 Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
 450 455 460
 Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
 465 470 475 480

Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
485 490 495

Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
500 505 510

Ile Gly Val Ala Ser Lys Leu Leu Ser
515 520

<210> 33
<211> 1566
<212> DNA
<213> Trifolium pratense

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gttgttgccct ccacaccaga attgttcaag ctcttcctcc aaacgcacga ggcaacttcc 300
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tcttaa 1566

<210> 34
<211> 521
<212> PRT
<213> Trifolium pratense

<400> 34
Met Leu Leu Glu Leu Ala Leu Gly Leu Leu Val Leu Ala Leu Phe Leu
1 5 10 15
His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu
20 25 30
Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
35 40 45
His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
50 55 60
Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
65 70 75 80

Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
 85 90 95
 Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
 100 105 110
 Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
 115 120 125
 Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
 130 135 140
 Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys Phe Leu
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 Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
 165 170 175
 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
 180 185 190
 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
 195 200 205
 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
 210 215 220
 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
 225 230 235 240
 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
 245 250 255
 Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
 260 265 270
 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Thr Glu Ile Lys
 275 280 285
 Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
 290 295 300
 Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
 305 310 315 320
 Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser
 325 330 335
 Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
 340 345 350
 Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
 355 360 365
 Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
 370 375 380
 Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
 385 390 395 400
 Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
 405 410 415
 Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Arg Pro Leu Asp Leu
 420 425 430

Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
435 440 445

Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
450 455 460

Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
465 470 475 480

Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
485 490 495

Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
500 505 510

Ile Gly Val Ala Ser Lys Leu Leu Ser
515 520

<210> 35
<211> 1563
<212> DNA
<213> Pisum sativum

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ttcagcacaa ggttccaaac ctctgccgta agacgcctca cttacgacaa ctctgtggcc 360
atggttccat tcggacctta ctggaagttc gtgaggaagc tcatcatgaa cgaccttctc 420
aacgccacca ccgtcaacga gctcaggcct ttgaggaccc aacagatccg caagttcctt 480
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aaatggacca acagcaccat ctccatgatg atgctcggcg aggctgagga gatcagagac 600
atcgctcgcg aggtccttaa gatcttcggc gaatacagcc tcaactgact catctggcct 660
ttgaagtatc tcaaggttgg aaagtatgag aagaggattg atgacatctt gaacaagttc 720
gacctgtgcg ttgaaagggt catcaagaag cgccgtgaga tcgtcagaag gagaaagaac 780
ggagaagttg ttgagggcga ggccagcggc gtcttcctcg acactttgct tgaattcgct 840
gaggacgaga ccattgggat caaaattacc aaggagcaaa tcaagggcct tgttgctgac 900
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gagacattcc gaatgcaccc accactccca gtggtcaaaa gaaagtgcac agaagagtgt 1140
gagattaatg ggtatgtgat cccagaggga gcattggttc ttttcaatgt ttggcaagta 1200
ggaaaggacc ccaataactg ggacagacca tcagaattcc gtcccagagag gttcttagaa 1260
actggcgctg aaggggaagc agggcctctt gatcttaggg gccagcattt ccaactcctc 1320
ccatttgggt ctgggaggag aatgtgccct ggtgtcaatt tggctacttc aggaatggca 1380
acacttcttg catctcttat ccaatgcttt gacctgcaag tgctgggccc tcaaggacaa 1440
atattgaaag gtgacgatgc caaagttagc atggaagaga gagctggcct caccgttcca 1500
agggcacata gtctcgtttg tgttccactt gcaaggatcg gcgttgcatc taaactcctt 1560
tct 1563

<210> 36
<211> 521
<212> PRT
<213> Pisum sativum

<400> 36
Met Leu Leu Glu Leu Ala Leu Gly Leu Phe Val Leu Ala Leu Phe Leu
1 5 10 15

His Leu Arg Pro Thr Pro Ser Ala Lys Ser Lys Ala Leu Arg His Leu
20 25 30

Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
35 40 45

His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
 50 55 60
 Lys Lys His Gly Pro Leu Phe Ser Leu Ser Phe Gly Ser Met Pro Thr
 65 70 75 80
 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Ala His
 85 90 95
 Glu Ala Thr Ser Phe Ser Thr Arg Phe Gln Thr Ser Ala Val Arg Arg
 100 105 110
 Leu Thr Tyr Asp Asn Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
 115 120 125
 Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
 130 135 140
 Val Asn Glu Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys Phe Leu
 145 150 155 160
 Arg Val Met Ala Gln Ser Ala Glu Ala Gln Lys Pro Leu Asp Val Thr
 165 170 175
 Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
 180 185 190
 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
 195 200 205
 Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys Tyr Leu
 210 215 220
 Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
 225 230 235 240
 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
 245 250 255
 Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Ala Ser Gly Val Phe
 260 265 270
 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
 275 280 285
 Ile Thr Lys Glu Gln Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
 290 295 300
 Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
 305 310 315 320
 Ile Asn Asn Pro Arg Val Leu Gln Lys Ala Arg Glu Glu Val Tyr Ser
 325 330 335
 Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
 340 345 350
 Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
 355 360 365
 Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
 370 375 380
 Tyr Val Ile Pro Glu Gly Ala Leu Val Leu Phe Asn Val Trp Gln Val
 385 390 395 400

Gly Lys Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
 405 410 415

Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
 420 425 430

Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
 435 440 445

Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
 450 455 460

Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
 465 470 475 480

Ile Leu Lys Gly Asp Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
 485 490 495

Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
 500 505 510

Ile Gly Val Ala Ser Lys Leu Leu Ser
 515 520

<210> 37
 <211> 1496
 <212> DNA
 <213> Trifolium repens

<400> 37
 tctcacttgc gtccacaccc aagtgcataa tcaaaagcac ttccgccacct cccaaaccct 60
 ccaagcccaa ggctcgtct tcccttcatt ggccaccttc acctcttaaa agataaactt 120
 ctccactatg caccatcga tctctccaaa aagcatggcc ccttattctc tctctccttc 180
 ggctccatgc caaccgtcgt tgcctccacc cctgagttgt tcaagctctt cctccaaacc 240
 cagcaggcaa cttccttcaa cacaaggttc caaacctctg ccataagaca cctcacttac 300
 gacaactctg tggccatggt tccattcgga ccttactgga agttcgtgag gaagctcatc 360
 atgaacgacc ttctcaacgc caccaccgtc aacaagctca ggcctttgag gacccaacag 420
 atccgcaagt tccttagggt tatggcccaa agcgcagagg cccagaagcc ccttgacgtc 480
 accgaggagc ttctcaaagt gaccaacagc accatctcca tgatgatgct cggcgaggct 540
 gaggagatca gagacatcgc tcgcgagggt cttaagatct tcggcgaata cagcctcact 600
 gacttcactt ggcctttgaa gtacctcaag gtttgaaaagt atgagaagag gattgatgac 660
 atcttgaaac agttcgaccc tgctgttgaa agggctcatca agaagcgccg tgagatcgtc 720
 agaaggagaa agaacggaga agttgttgag ggcgaggcca gcggcgtctt cctcgacact 780
 ttgcttgaat tcgctgagga cgagaccatg gagatcaaaa ttaccaagga gcaaatcaag 840
 ggccttggtg tcgacttttt ctctgcaggg acagattcca cagcgtgtgt aacagagtgg 900
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 agtggttggt gcaaagatag actcgttgac gaagttgaca ctcaaaacct tccttacatt 1020
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 aatgtttggc aagtaggaag ggaccccaaa tactgggaca gaccatcaga atcccgtccc 1200
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 ggccctcaag gacaaatatt gaaaggtgat gatgccaaag ttagcatgga agagagagct 1440
 ggcctcacag ttccaagggc acatagtctc gtttgtgttc cacttgcaag gatcgg 1496

<210> 38
 <211> 498
 <212> PRT
 <213> Trifolium repens

<400> 38
 Ser His Leu Arg Pro Thr Pro Ser Ala Ile Ser Lys Ala Leu Arg His
 1 5 10 15

Leu Pro Asn Pro Pro Ser Pro Arg Pro Arg Leu Pro Phe Ile Gly His
 20 25 30
 Leu His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Pro Ile Asp Leu
 35 40 45
 Ser Lys Lys His Gly Pro Leu Phe Ser Leu Ser Phe Gly Ser Met Pro
 50 55 60
 Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr
 65 70 75 80
 His Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg
 85 90 95
 His Leu Thr Tyr Asp Asn Ser Val Ala Met Val Pro Phe Gly Pro Tyr
 100 105 110
 Trp Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr
 115 120 125
 Thr Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys Phe
 130 135 140
 Leu Arg Val Met Ala Gln Ser Ala Glu Ala Gln Lys Pro Leu Asp Val
 145 150 155 160
 Thr Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met
 165 170 175
 Leu Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys
 180 185 190
 Ile Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys Tyr
 195 200 205
 Leu Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys
 210 215 220
 Phe Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val
 225 230 235 240
 Arg Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Ala Ser Gly Val
 245 250 255
 Phe Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile
 260 265 270
 Lys Ile Thr Lys Glu Gln Ile Lys Gly Leu Val Val Asp Phe Phe Ser
 275 280 285
 Ala Gly Thr Asp Ser Thr Ala Val Val Thr Glu Trp Ala Leu Ala Glu
 290 295 300
 Leu Ile Asn Asn Pro Arg Val Leu Gln Lys Ala Arg Glu Glu Val Tyr
 305 310 315 320
 Ser Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn
 325 330 335
 Leu Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro
 340 345 350
 Pro Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn
 355 360 365

Gly Tyr Val Ile Pro Glu Gly Ala Leu Val Leu Phe Asn Val Trp Gln
 370 375 380

Val Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Ser Arg Pro
 385 390 395 400

Glu Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp
 405 410 415

Leu Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg
 420 425 430

Met Cys Pro Gly Val Ser Leu Ala Thr Ser Gly Met Ala Thr Leu Leu
 435 440 445

Ala Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly
 450 455 460

Gln Ile Leu Lys Gly Asp Asp Ala Lys Val Ser Met Glu Glu Arg Ala
 465 470 475 480

Gly Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala
 485 490 495

Arg Ile

<210> 39
 <211> 1501
 <212> DNA
 <213> Trifolium repens

<400> 39
 tggtttctgca cttgcgtccc acaccactg caaaatcaaa agcacttcgc catctcccaa 60
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 aacttctcca ctacgcactc atcgacctct ccaaaaaaca tgggtccctta ttctctctct 180
 actttggctc catgccaacc gttgttgctt ccacaccaga attgttcaag ctcttctctc 240
 aaacgcacga ggcaacttcc ttcaacacaa ggttccaaac ctacagccata agacgcctca 300
 cctacgacaa ctctgtggcc atgggttccat tcggacctta ctggaagttc gtgaggaagc 360
 tcatcatgaa cgaccttctc aacgccacca ccgtcaacaa gctcaggcct ttgaggacct 420
 aacagatccg caagtctctt aggggttatgg cccaaagcgc agaggcccag aagccccttg 480
 acgtcaccga ggagcttctc aaatggacca acagcaccat ctccatgatg atgctcggcg 540
 aggctgagga gatcagagac atcgctcgcg aggttcttaa gatcttcggc gaatacagcc 600
 tcaactgactt catctggcct ttgaagtatc tcaagggttg aaagtatgag aagaggattg 660
 atgacatctt gaacaagtgc gacctgtcg ttgaaagagt catcaagaag cgccgtgaga 720
 tcgtcagaag gagaaagaac ggagaagttg ttgaggcgga ggccagcggc gtcttctctc 780
 acactttgct tgaattcgct gaggacgaga ccatggagat caaaattacc aaggagcaaa 840
 tcaagggcct tgttgctgac tttttctctg cagggacaga ttccacagcg gtggcaacag 900
 agtgggcatt ggcagagctc atcaacaatc ccaagggtgt gcaaaaggct cgtgaggagg 960
 cctacagtgt tgtgggcaaa gatagactcg ttgacgaagt tgacactcaa aaccttctct 1020
 acattagggc cattgtgaag gagacattcc gaatgcaccc accactcca gtggtcaaaa 1080
 gaaagtgcac agaagagtgt gggattaatg ggtatgtgat ccagaggga gcattggttc 1140
 ttttcaatgt ttggcaagta ggaagggacc ccaataactg ggacagacca tcagaattcc 1200
 gtcccagag gttcttagaa actggtgctg aaggggaagc agggcctctt gatcttaggg 1260
 gccagcattt ccaactcctc ccatttgggt ctgggaggag aatgtgccct ggtgtcaatt 1320
 tggctacttc aggaatggca acacttcttg catctcttat ccaatgcttt gacctgcaag 1380
 tgctgggccc tcaaggacaa atattgaaag gtgatgatgc caaagttagc atggaagaga 1440
 gagctggcct cacagttcca agggcacata gtctcgtttg tgttccactt gcaaggatcg 1500
 g 1501

<210> 40
 <211> 499
 <212> PRT
 <213> Trifolium repens

<400> 40

Phe Leu His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg
 1 5 10 15
 His Leu Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly
 20 25 30
 His Leu His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp
 35 40 45
 Leu Ser Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met
 50 55 60
 Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln
 65 70 75 80
 Thr His Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile
 85 90 95
 Arg Arg Leu Thr Tyr Asp Asn Ser Val Ala Met Val Pro Phe Gly Pro
 100 105 110
 Tyr Trp Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala
 115 120 125
 Thr Thr Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys
 130 135 140
 Phe Leu Arg Val Met Ala Gln Ser Ala Glu Ala Gln Lys Pro Leu Asp
 145 150 155 160
 Val Thr Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met
 165 170 175
 Met Leu Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu
 180 185 190
 Lys Ile Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys
 195 200 205
 Tyr Leu Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn
 210 215 220
 Lys Phe Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile
 225 230 235 240
 Val Arg Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Ala Ser Gly
 245 250 255
 Val Phe Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu
 260 265 270
 Ile Lys Ile Thr Lys Glu Gln Ile Lys Gly Leu Val Val Asp Phe Phe
 275 280 285
 Ser Ala Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala
 290 295 300
 Glu Leu Ile Asn Asn Pro Lys Val Leu Gln Lys Ala Arg Glu Glu Ala
 305 310 315 320
 Tyr Ser Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln
 325 330 335
 Asn Leu Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His
 340 345 350

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099
1990	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099

34

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 44
cctctcggga cggaattctg atggt

25

<210> 45
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 45
gcggtgcacg ggcggactct tcttc

25

<210> 46
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 46
cgccaatac gcaaaccgcc tctcc

25

<210> 47
<211> 1501
<212> DNA
<213> Beta vulgaris

<400> 47
tgtttctgca cttgcgtccc acacccactg caaaatcaaa agcacttcgc catctcccaa 60
acccaccaag cccaaagcct cgtcttccct tcataggaca ccttcatctc ttaaaagaca 120
aacttctcca ctacgcactc atcgacctct ccaaaaaaca tggctccctta ttctctctct 180
actttggctc catgccaacc gttgttgctt ccacaccaga attgttcaag ctcttcctcc 240
aaacgcacga ggcaacttcc ttcaacacaa ggttccaaac ctacgccata agacgcctca 300
cctatgatag ctacgtggcc atgggttccct tcggacctta ctggaagttc gtgaggaagc 360
tcatcatgaa cgaccttctc aacgccacca ctgtaaaciaa gttgaggcct ttgaggacct 420
aacagatccg caagttcctt aggggttatgg cccaaggcgc agaggcacag aagccccttg 480
acttgaccga ggagcttctg aaatggacca acagcaccat ctccatgatg atgctcggcg 540
aggctgagga gatcagagac atcgctcgcg aggttcttaa gatctttggc gaatacagcc 600
tactgactt catctggcca ttgaagcatc tcaaggttgg aaagtatgag aagaggatcg 660
acgacatctt gaacaagttc gacctgtctg ttgaaagagt catcaagaag cgccgtgaga 720
tcgtgaggag gaaaaagaac ggagaggatg ttgagggatg ggtcagcggg gttttccttg 780
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tcaagggctc tgttctcgac tttttctcgg caggaacaga ctccacagcg gtggcaacag 900
agtgggcatt ggcagaactc atcaacaatc ctaagggtgtt ggaaaaggct cgtgaggagg 960
tctacagtgt tgtgggaaag gacagacttg tggacgaagt agacactcaa aaccttcctt 1020
acattagagc aatcgtgaag gagacattcc gcatgcaccc gccactccca gtggtcaaaa 1080
gaaagtgcac agaagagtgt gagattaatg gatatgtgat cccagaggga gcattgatc 1140
tcttcaatgt atggcaagta ggaagagacc cttaaatactg ggacagacca tcggagttcc 1200
gtcctgagag gttcctagag acaggggctg aaggggaagc aaggttctct gatcttaggg 1260
gacaacattt tcaacttctc ccatttgggt ctgggaggag aatgtgccct ggagtcaatc 1320
tggtacttcc gggaaatggca acacttcttg catctcttat tcagtgtctt gacttgcaag 1380
tgctgggtcc acaaggacag atattgaagg gtggtgacgc caaagttagc atggaagaga 1440
gagccggcct cactgttcca agggcacata gtcttgtctg tgttccactt gcaaggatcg 1500
g 1501

<210> 48
<211> 499

<212> PRT
<213> Beta vulgaris

<400> 48

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Phe Leu His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg
 1           5           10           15

His Leu Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly
          20           25           30

His Leu His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp
          35           40           45

Leu Ser Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met
          50           55           60

Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln
          65           70           75           80

Thr His Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile
          85           90           95

Arg Arg Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro
          100          105          110

Tyr Trp Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala
          115          120          125

Thr Thr Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys
          130          135          140

Phe Leu Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp
          145          150          155          160

Leu Thr Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met
          165          170          175

Met Leu Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu
          180          185          190

Lys Ile Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys
          195          200          205

His Leu Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn
          210          215          220

Lys Phe Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile
          225          230          235          240

Val Arg Arg Arg Lys Asn Gly Glu Asp Val Glu Gly Glu Val Ser Gly
          245          250          255

Val Phe Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu
          260          265          270

Ile Lys Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe
          275          280          285

Ser Ala Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala
          290          295          300

Glu Leu Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val
          305          310          315          320

Tyr Ser Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln
          325          330          335

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Asn Leu Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His
 340 345 350
 Pro Pro Leu Pro Val Val Lys Arg Lys Cys Ile Glu Glu Cys Glu Ile
 355 360 365
 Asn Gly Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp
 370 375 380
 Gln Val Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg
 385 390 395 400
 Pro Glu Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Arg Leu Leu
 405 410 415
 Asp Leu Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg
 420 425 430
 Arg Met Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu
 435 440 445
 Leu Ala Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln
 450 455 460
 Gly Gln Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg
 465 470 475 480
 Ala Gly Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu
 485 490 495

Ala Arg Ile

<210> 49
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 49
 gaattcgcgg ccgctctaga actagtggat

30

<210> 50
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 50
 gaattcgcgg ccgcgaattg ggtaccgggc

30

<210> 51
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 51
 gcaaacgaag acaaatggga gatgata

27

<210> 52
 <211> 1801
 <212> DNA
 <213> Glycine max

<220>
 <221> intron
 <222> (895)..(1112)

<400> 52
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 ccaagtgcaa aatcaaaagc acttcgccac ctcccaaacc ctccaagccc aaagcctcgt 120
 cttcccttca ttggccaacct tcacctctta aaagataaac ttctccacta tgcactcatc 180
 gatctctcca aaaagcatgg ccccttattc tctctctcct tcgggtccat gccaacccgtc 240
 gttgcctcca cccctgagtt gttcaagctc ttctccaaa cccacgaggc aacttccttc 300
 aacacaagggt tccaaacctc tgccataaga cgctcactt acgacaactc tgtggccatg 360
 gttccattcg gaccttactg gaagttcgtg aggaagctca tcatgaacga ccttctcaac 420
 gccaccaccg tcaacaagct caggcctttg aggacccaac agatccgcaa gttccttagg 480
 gttatggccc aaagcgcaga ggcccagaag ccccttgacg tcaccgagga gcttctcaaa 540
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 gctcgcgagg ttcttaagat cttcggcgaa tacagcctca ctgacttcat ctggcctttg 660
 aagtatctca aggttggaag gtatgagaag aggattgatg acatcttgaa caagttcgac 720
 cctgtcgttg aaagggatcat caagaagcgc cgtgagatcg tcagaaggag aaagaacgga 780
 gaagttgttg agggcgaggc cagcggcgtc ttctcgcaga ctttgcttga attcgtgag 840
 gacgagacca tggagatcaa aattaccaag gagcaaatca agggccttgt tgtcgtaagt 900
 ttcttcttct tctctactt tattactttc tttcattcat catatgtatt ggcattaaat 960
 agtatactat atgagaaaat atgttacgca ctacaggtgt aaagatatgt ggtgtttttt 1020
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 aaactaatta attctcaatt ttgggtatgt aggacttttt ctctgcaggg acagattcca 1140
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 aggtcgtgga ggaggtctac agtgttgttg gcaaagatag actcgttgac gaagttgaca 1260
 ctcaaaacct tccttacatt agggccattg tgaaggagac attccgaatg caccaccac 1320
 tcccagtggt caaaagaaag tgcacagaag agtgtgagat taatgggtat gtgatcccag 1380
 agggagcatt gggtcttttc aatgtttggc aagtaggaag ggaccccaaa tactgggaca 1440
 gaccatcaga attcgtccc gagaggttct tagaaactgg tgctgaaggg gaagcagggc 1500
 ctcttgatct taggggccag catttccaac tcctcccatt tgggtctggg aggagaatgt 1560
 gccctgggtg caatttggct acttcaggaa tggcaaacact tcttgcatct cttatccaat 1620
 gctttgacct gcaagtgtcg ggccctcaag gacaaatatt gaaaggtgat gatgccaaag 1680
 ttagcatgga agagagagct ggcctcacag ttccaagggc acatagtctc gtttgtgttc 1740
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 c 1801

<210> 53
 <211> 1900
 <212> DNA
 <213> Glycine max

<220>
 <221> intron
 <222> (947)..(1082)

<400> 53
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 aaaatcaaaa gcacttcgcc atctcccaaa cccaccaagc ccaaagcctc gtcttccctt 180
 cataggacac cttcatctct taaaagacaa acttctccac tacgcaactc tcgacctctc 240
 caaaaaacat ggtcccttat tctctctcta ctttggtctc atgccaaccg ttgttgcttc 300
 cacaccagaa ttgttcaagc tcttctcca aacgcacgag gcaacttcct tcaacacaag 360
 gttccaaacc tcagccataa gacgcctcac ctatgatagc tcagtggcca tggttccctt 420
 cggaaccttac tggaagtctg tgaggaagct catcatgaac gaccttcca acgccaccac 480
 tgtaaacaaag ttgaggcctt tgaggaccca acagaccgc aagttcctta ggttatggc 540
 ccaaggcgca gaggcacaga agccccttga cttgaccgag gagcttctga aatggacca 600
 cagcaccatc tccatgatga tgctcggcga ggtgaggag atcagagaca tcgctcgca 660
 ggttcttaag atctttggcg aatacagcct cactgacttc atctggccat tgaagcatct 720
 caagggttga aagtatgaga agaggatcga cgacatcttg aacaagttcg accctgtcgt 780

tgaaaggggtc	atcaagaagc	gccgtgagat	cgtgaggagg	agaaagaacg	gagaggttgt	840
tgaggggtgag	gtcagcgggg	ttttccttga	cacttttgctt	gaattcgctg	aggatgagac	900
catggagatc	aaaatcacca	aggaccacat	cgaggggtcctt	gttgctcgtga	gtttcctgct	960
tcattcattg	atcgaaatat	gcagtatttt	gttaacaaga	gatcgagaat	tgacatttat	1020
atattcatgt	ggtggcaatt	aattaacggt	acgcattctt	aatcgatatt	gtgtatgtgc	1080
aggacttttt	ctcggcagga	acagactcca	cagcgggtggc	aacagagtgg	gcattggcag	1140
aactcatcaa	caatcctaag	gtgttggaag	aggctcgtga	ggaggtctac	agtgttggtg	1200
gaaaggacag	acttggtggac	gaagttgaca	ctcaaaacct	tccttacatt	agagcaatcg	1260
tgaaggagac	attccgcatg	cacccgccac	tcccagtggt	caaaagaaaag	tgacacagaag	1320
agtgtgagat	taatggatat	gtgatcccag	agggagcatt	gattctcttc	aatgtatggc	1380
aagtaggaag	agaccccaaa	tactgggaca	gaccatcgga	gttccgtcct	gagaggttcc	1440
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ttctcccatt	tgggtctggg	aggagaatgt	gccctggagt	caatctggct	acttcgggaa	1560
tggcaacact	tcttgcatct	cttattcagt	gcttcgactt	gcaagtgtctg	ggtccacaag	1620
gacagatatt	gaaggggtgt	gacgccaaag	ttagcatgga	agagagagcc	ggcctcactg	1680
ttccaagggc	acatagtctt	gtctgtgttc	cacttgcaag	gatcggcggt	gcactctaac	1740
tcctttctta	attaagatca	tcgtcatcat	catcatatat	aatatttact	ttttgtgtgt	1800
tgataatcat	catttcaata	aggtctcgtt	catctacttt	ttatgaagta	tataagccct	1860
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<210> 54
 <211> 1501
 <212> DNA
 <213> Lupinus albus

<400> 54
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 aacttctcca ctacgcactc atcgacctct ccaaaaaaca tggctccctta ttctctctct 180
 actttggctc catgccaaac gttgttgctc ccacaccaga attgttcaag ctcttccctoc 240
 aaacgcagca ggcaacttcc ttcaacacaa ggttccaaac ctccagccata agacgcctca 300
 cctatgatag ctacgtggcc agggttccct tcggacctta ctggaagttc gtgaggagc 360
 tcatcatgaa cgaccttctt aacgccacca ctgtaaacaa gttgaggcct ttgaggaccc 420
 aacagatccg caagttcctt agggttatgg cccaaggcgc agaggcacag aagcccttg 480
 acttgaccga ggagcttctg aaatggacca acagcaccat ctccatgatg atgctcggcg 540
 aggctgagga gatcagagac atcgctcgcg aggttcttaa gatctttggc gaatacacgcc 600
 tcaactgactt catctggcca ttgaagcatc tcaaggttgg aaagtatgag aagaggatcg 660
 acgacatctt gaacaagttc gacctgtctg ttgaaagagt catcaagaag cgccgtgaga 720
 tcgtgaggag gagaaagaac ggagaggttg ttgaggggtga ggtcagcggg gttctccttg 780
 acactttgct tgaattcgct gaggatgaga ccatggagat caaaatcacc aaggaccaca 840
 tcaagggtct tgttgctgac tttttctcgg caggaacaga ctccacagcg gtggcaacag 900
 agtgggcatt ggcagaactc atcaacaatc ctaaggtgtt ggaaagggtc cgtgaggagg 960
 tctacagtgt tgtgggaaag gacagacttg tggacgaagt tgacactcaa aaccttccct 1020
 acattagagc aatcgtgaag gagacattcc gcatgcaccc gccactccca gtggtcaaaa 1080
 gaaagtgcac agaagagtgt gagattaatg gatatgtgat cccagaggga gcattgattc 1140
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 gtccctgagag gttccttagag acagaggctg aagggggaagc aaggcctctt gatcttaggg 1260
 gacaacattt tcaacttctc ccatttgggt ctgggaggag aatgtgccct ggagtcattc 1320
 tggctacttc gggaatggca acacttcttg catctcttat tcagtgtctt gacttgcaag 1380
 tgctgggtcc acaaggacag atattgaagg gtggtgacgc caaagttagc atggaagaga 1440
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 g 1501

<210> 55
 <211> 499
 <212> PRT
 <213> Lupinus albus

<400> 49
 Phe Leu His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg
 1 5 10 15
 His Leu Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly
 20 25 30

His Leu His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp
 35 40 45
 Leu Ser Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met
 50 55 60
 Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln
 65 70 75 80
 Thr His Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile
 85 90 95
 Arg Arg Leu Thr Tyr Asp Ser Ser Val Ala Arg Val Pro Phe Gly Pro
 100 105 110
 Tyr Trp Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala
 115 120 125
 Thr Thr Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys
 130 135 140
 Phe Leu Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp
 145 150 155 160
 Leu Thr Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met
 165 170 175
 Met Leu Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu
 180 185 190
 Lys Ile Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys
 195 200 205
 His Leu Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn
 210 215 220
 Lys Phe Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile
 225 230 235 240
 Val Arg Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly
 245 250 255
 Val Leu Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu
 260 265 270
 Ile Lys Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe
 275 280 285
 Ser Ala Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala
 290 295 300
 Glu Leu Ile Asn Asn Pro Lys Val Leu Glu Arg Ala Arg Glu Glu Val
 305 310 315 320
 Tyr Ser Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln
 325 330 335
 Asn Leu Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His
 340 345 350
 Pro Pro Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile
 355 360 365
 Asn Gly Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp
 370 375 380

Gln Val Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg
385 390 395 400

Pro Glu Arg Phe Leu Glu Thr Glu Ala Glu Gly Glu Ala Arg Pro Leu
405 410 415

Asp Leu Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg
420 425 430

Arg Met Cys Pro Gly Val Ile Leu Ala Thr Ser Gly Met Ala Thr Leu
435 440 445

Leu Ala Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln
450 455 460

Gly Gln Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg
465 470 475 480

Ala Gly Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu
485 490 495

Ala Arg Ile

<210> 56
<211> 1501
<212> DNA
<213> Medicago sativa

<400> 56
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acccaccaag cccaaagcct cgtcttccct tcataggaca ccttcattctc ttaaaagaca 120
aactttctcca ctacgcactc atcgacctct ccaaaaaaca tgggtccctta ttctctctct 180
acttttggtc catgccaaacc gttgttgctt ccacaccaga attgttcaag ctcttccttc 240
aaacgcacga ggcaacttcc ttcaacacaa ggttccaaac ctacagccata agacgcctca 300
cctatgatag ctacgtggcc atggctccct tcggacctta ctggaagttc gtgaggaagc 360
tcatcatgaa cgaccttctc aacgccacca ctgtaaaciaa gttgaggcct ttgaggaccc 420
aacagatccg caagttcctt agggttatgg cccaaggcgc agaggcacag aagccccttg 480
acttgaccga ggagcttctg aaatggacca acagcaccac ctccatgatg atgctcggcg 540
aggctgagga gatcagagac atcgcccgcg aggttcttaa gatctttggc gaatacagcc 600
tactgactt catccggcca ttgaagcatc tcaagggttg aaagtatgag aagaggatcg 660
acgacatctt gaacaagttc gacctgtctg ttgaaagagt catcaagaag cgccgtgaga 720
tcgtgaggag gagaaagaac ggagaggttg ttgagggtga ggtcagcggg gttttccttg 780
acactttgct tgaattcgct gaggtatgaga ccacggagat caaaatcacc aaggaccaca 840
tcaagggtct tgttgctgac tttttctcgg caggaacaga ctccacagcg gtggcaacag 900
agtgggcatt ggcagaactc atcaacaatc ctaagggtgt ggaaaaggct cgtgaggagg 960
tctacagtgt tgtgggaaaag gacagacttg tggacgaagt tgacactcaa aaccttctt 1020
acattagagc aatcgtgaag gagacattcc gcatgcaccc gccactccca gtggtcaaaa 1080
gaaagtgcac agaagagtgt gagattaatg gatattgat cccagagggg gcattgattc 1140
tcttcaatgt atggcaagta ggaagagact ccaaatactg ggacagacca tcggagttcc 1200
gtcctgagag gttcctagag acaggggctg aaggggaagc aaggcctctt gatcttaggg 1260
gacaacattt tcaacttctc ccatttggtt ctgggaggag aatgtgccct ggagtcaatc 1320
tggtacttcc gggaatggca acacttcttg catctcttat tcagtgtttt gacttgcaag 1380
tgctgggtcc acaaggacag atattgaagg gtggtgacgc caaagttagc atggaagaga 1440
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g 1501

<210> 57
<211> 499
<212> PRT
<213> Medicago sativa

<400> 57
Phe Leu His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg
1 5 10 15

His Leu Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly
 20 25 30
 His Leu His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp
 35 40 45
 Leu Ser Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met
 50 55 60
 Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln
 65 70 75 80
 Thr His Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile
 85 90 95
 Arg Arg Leu Thr Tyr Asp Ser Ser Val Ala Met Ala Pro Phe Gly Pro
 100 105 110
 Tyr Trp Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala
 115 120 125
 Thr Thr Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys
 130 135 140
 Phe Leu Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp
 145 150 155 160
 Leu Thr Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Thr Ser Met Met
 165 170 175
 Met Leu Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu
 180 185 190
 Lys Ile Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Arg Pro Leu Lys
 195 200 205
 His Leu Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn
 210 215 220
 Lys Phe Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile
 225 230 235 240
 Val Arg Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly
 245 250 255
 Val Phe Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Thr Glu
 260 265 270
 Ile Lys Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe
 275 280 285
 Ser Ala Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala
 290 295 300
 Glu Leu Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val
 305 310 315 320
 Tyr Ser Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln
 325 330 335
 Asn Leu Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His
 340 345 350
 Pro Pro Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile
 355 360 365

Asn Gly Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp
 370 375 380

Gln Val Gly Arg Asp Ser Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg
 385 390 395 400

Pro Glu Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Arg Pro Leu
 405 410 415

Asp Leu Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg
 420 425 430

Arg Met Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu
 435 440 445

Leu Ala Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln
 450 455 460

Gly Gln Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg
 465 470 475 480

Ala Gly Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu
 485 490 495

Ala Arg Ile

<210> 58
 <211> 1501
 <212> DNA
 <213> *Medicago sativa*

<400> 58
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 aacttctcca ctacgcactc atcgacctct ccaaaaaaca tggcccctta ttctctctct 180
 actttggctc catgccaaacc gttgttgccct ccacaccaga attgttcaag ctcttcctcc 240
 aaacgcacga ggcaacttcc ttcaacacaa gggtccaaac ctacagccata agacgcctca 300
 cctatgatag ctcatgtggc atgggtccct tgggacctta ctggaagttc gtgagggaagc 360
 tcatcatgaa cgaccttctc aacgccacca ctgtaaaciaa gttgaggcct ttgaggaccc 420
 aacagatccg caagctcctt aggggttatgg cccaaggcgc agaggcacag aagccccttg 480
 acttgaccga ggagcttctg aaatggacca acagcaccat ctccatgatg atgctcggcg 540
 aggtgagga gatcagagac atcgctcgcg aggttcttaa gatctttggc gaatacagcc 600
 tcaactgact catctggcca ttgaagcatc tcaagggttg aaagtatgag aagaggatcg 660
 acgacatctt gaacaagttc gaccctgtcg ttgaaagagt catcaagaag cgcctgaga 720
 tcgtgaggag gagaagaac ggagaggtta ttgagggtga ggtcagcggg gttttccttg 780
 acactttgct tgaattcgct gaggatgaga ccacggagat caaaatcacc aaggaccaca 840
 tcaagggtct tgttgctcgac ttttctcgg caggaaacaga ctccacagcg gtggcaacag 900
 agtgggcatt ggcagaactc atcaacaatc ctaagggtgt ggagaaggct cgtgaggagg 960
 tctacagtgt tgtgggaaag gacagacttg tggacgaagt tgacactcaa aaccttctt 1020
 acattagagc aatcgtgaag gagacattcc gcatgcaccc gccactccca gtggtcaaaa 1080
 gaaagtgcac agaagagtgt gagattaatg gatattgatg cccagaggga gcattgatc 1140
 tcttcaatgt atggcaagta ggaagagacc ccaaatactg ggacagacca tcggagttcc 1200
 gtcctgagag gttcctagag acaggggctg aaggggaagc aaggcctctt gatcttaggg 1260
 gacaacattt tcaacttctc ccatttgggt ctgggaggag aatgtgccct ggagtcaatc 1320
 tggctacttc gggaatggca acacttcttg catctcttat tcagtgtctt gacttgcaag 1380
 tgcgtgggtcc acaaggacag atattgaagg gtggtgacgc caaagttagc atggaagaga 1440
 gggccggcct cactgttcca agggcacata gtcttgctg tgttccactt gcaaggatcg 1500
 g 1501

<210> 59
 <211> 499
 <212> PRT
 <213> *Medicago sativa*

<400> 59

Phe Leu His Leu Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg
 1 5 10 15
 His Leu Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly
 20 25 30
 His Leu His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp
 35 40 45
 Leu Ser Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met
 50 55 60
 Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln
 65 70 75 80
 Thr His Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile
 85 90 95
 Arg Arg Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro
 100 105 110
 Tyr Trp Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala
 115 120 125
 Thr Thr Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys
 130 135 140
 Leu Leu Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp
 145 150 155 160
 Leu Thr Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met
 165 170 175
 Met Leu Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu
 180 185 190
 Lys Ile Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys
 195 200 205
 His Leu Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn
 210 215 220
 Lys Phe Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile
 225 230 235 240
 Val Arg Arg Arg Lys Asn Gly Glu Val Ile Glu Gly Glu Val Ser Gly
 245 250 255
 Val Phe Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Thr Glu
 260 265 270
 Ile Lys Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe
 275 280 285
 Ser Ala Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala
 290 295 300
 Glu Leu Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val
 305 310 315 320
 Tyr Ser Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln
 325 330 335
 Asn Leu Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His
 340 345 350

Pro Pro Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile
355 360 365

Asn Gly Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp
370 375 380

Gln Val Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg
385 390 395 400

Pro Glu Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Arg Pro Leu
405 410 415

Asp Leu Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg
420 425 430

Arg Met Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu
435 440 445

Leu Ala Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln
450 455 460

Gly Gln Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg
465 470 475 480

Ala Gly Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu
485 490 495

Ala Arg Ile

<210> 60
<211> 1497
<212> DNA
<213> Beta vulgaris

<400> 60
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accaagccca aagcctcgtc ttcccttcac aggcacacct catctcttaa aagacaaact 120
tctccactac gcaactcatcg acctctccaa aaaacatggc cccttattct ctcaactactt 180
tggtcccatg ccaaccggttg ttgcctccac accagaattg ttcaagctct tcctccaaac 240
gaacgaggca acttccttca acacaagggt ccaaacctca gccataagac gcctcaccta 300
tgatagctca gtggccatgg ttcccttcgg accttactgg aagttcgtga ggaagctcat 360
catgaacgac cttctcaacg ccaccactgt aaacaagttg aggcctttga ggaccaaca 420
gatccgcaag ttctttaggg ctatggccca aggcgcagag gcacggaagc cccttgactt 480
gaccgaggag cttctgaaat gggccaacag caccatctcc atgatgatgc tcggcgaggc 540
tgaggagatc agagacatcg ctgcgaggtt tcttaagatc tttggcgaat acagcctcac 600
tgacttcac tggccattga agcatctcaa ggttgaaaag tatgagaaga ggatcgacga 660
catcttgaac aagttcgacc ctgtcggttg aagagtcac aagaagcgcc gtgagatcgt 720
gaggaggaga aagaacggag aggttggtga gggtaggttc agcgggggtt tccttgacac 780
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 Arg Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr
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 225 230 235 240
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 35 40 45
 His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Xaa Ile Asp Leu Ser
 50 55 60
 Lys Lys His Gly Pro Leu Phe Ser Xaa Xaa Phe Gly Ser Met Pro Thr
 65 70 75 80
 Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Xaa Xaa
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 Glu Ala Thr Ser Phe Xaa Thr Arg Phe Gln Thr Ser Ala Xaa Arg Xaa
 100 105 110
 Leu Thr Tyr Asp Xaa Xaa Val Ala Xaa Xaa Pro Xaa Gly Pro Tyr Trp
 115 120 125
 Xaa Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
 130 135 140
 Val Asn Xaa Leu Arg Pro Leu Arg Thr Gln Gln Ile Arg Lys Xaa Leu
 145 150 155 160
 Arg Xaa Met Ala Gln Xaa Ala Glu Ala Xaa Lys Pro Leu Asp Xaa Thr
 165 170 175
 Glu Glu Leu Leu Lys Trp Xaa Asn Ser Thr Xaa Ser Met Met Xaa Leu
 180 185 190
 Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
 195 200 205
 Xaa Gly Glu Tyr Ser Leu Thr Asp Phe Ile Xaa Pro Leu Lys Xaa Leu
 210 215 220

Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
 225 230 235 240
 Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Xaa Ile Val Arg
 245 250 255
 Arg Arg Xaa Asn Gly Glu Xaa Xaa Glu Gly Glu Xaa Ser Gly Val Xaa
 260 265 270
 Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Xaa Glu Ile Lys
 275 280 285
 Ile Thr Lys Xaa Xaa Ile Lys Gly Leu Val Val Asp Xaa Phe Ser Ala
 290 295 300
 Gly Xaa Asp Ser Thr Ala Xaa Xaa Thr Glu Trp Ala Leu Ala Glu Leu
 305 310 315 320
 Ile Asn Asn Pro Xaa Val Leu Xaa Xaa Ala Arg Glu Glu Xaa Tyr Ser
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 Val Val Gly Lys Asp Xaa Leu Val Asp Glu Val Asp Thr Gln Asn Leu
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 Arg Gly Xaa His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Xaa Met
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 Cys Pro Gly Val Xaa Leu Ala Thr Ser Gly Xaa Ala Thr Leu Leu Ala
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 Ile Leu Lys Gly Xaa Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
 485 490 495
 Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
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